



The image shows the NCBI Nucleotide search interface. At the top, there is a sequence viewer window displaying a DNA sequence with various nucleotides highlighted in different colors (A, T, C, G) and some gaps. Below the sequence viewer is a navigation bar with links: PubMed, Nucleotide, Protein, Genome, Structure, PMC, Taxonomy, OMIM, and Books. A search bar is present with the text 'Search Nucleotide for' and buttons for 'Go' and 'Clear'. Below the search bar are buttons for 'Limits', 'Preview/Index', 'History', 'Clipboard', and 'Details'. At the bottom of the search bar are buttons for 'Display' (set to 'default'), 'Show' (set to 20), 'Send to', 'File', and 'Get Subsequence'.

□1: AK024798. Homo sapiens cDNA...[gi:10437188]

Links

**LOCUS** AK024798 1577 bp mRNA linear PRI 29-SEP-2000  
**DEFINITION** Homo sapiens cDNA: FLJ21145 fis, clone CAS08741.  
**ACCESSION** AK024798  
**VERSION** AK024798.1 GI:10437188  
**KEYWORDS** oligo capping; fis (full insert sequence).  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (sites)  
**AUTHORS** Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,  
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,  
Nakamura,Y., Isogai,T. and Sugano,S.  
**TITLE** NEDO human cDNA sequencing project  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 1577)  
**AUTHORS** Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,  
Shibahara,T., Tanaka,T. and Nakamura,Y.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure Analysis, Human  
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,  
Japan (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)  
**COMMENT** NEDO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan; cDNA full insert  
sequencing: Research Association for Biotechnology; cDNA library  
construction, 5'- & 3'-end one pass sequencing: Department of  
Virology and Human Genome Center, Institute of Medical Science,  
University of Tokyo (partly supported by Science and Technology  
Agency).  
**FEATURES** Location/Qualifiers  
**source** 1..1577  
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LVADGCCNLQKQIQTQLFGVPPVVALNVFKTDTRAEIFLVCCELAKRAGAFDAVPCYH  
WSVGGKGSVDLARAVREAASKRSRFQFLYDVQVPIVDKIMTIAQAVYGAKDIELSPEA  
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BASE COUNT      424 a      336 c      420 g      397 t  
ORIGIN

VGTMSTMPGLPTRPCFYDIDLDTEQVKGLF"

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121 gaaggatggt ggtggccagt gacaaaagcg ggcagcctgt gacagcagat gatgggggg  
181 tgacagggtgc tttgcacgtt ttgatgaaag atgcaataaa accaaacctg atgcagaccc  
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1501 tccactctca agttttctac ttgtctttt aactgaaaat aaacatggat ctagaaaacc  
1561 aaaaaaaaaaaaaaaa aaaaaaaaaaaa

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Revised: July 5, 2002.

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(FILE 'HOME' ENTERED AT 15:55:28 ON 23 JAN 2003)

FILE 'MEDLINE, CAPLUS' ENTERED AT 15:55:33 ON 23 JAN 2003

L1 4225 S TETRAHYDROFOLATE DEHYDROGENASE  
L2 0 S L1 AND CYCLOHYDRO  
L3 40 S L1 AND ("REVIEW" OR "REVIEWS")  
L4 40 DUP REM L3 (0 DUPLICATES REMOVED)  
L5 51 S L1 AND CYCLOHYDRO?  
L6 44 DUP REM L5 (7 DUPLICATES REMOVED)